Docket No. PU4928USw

IAN 2 7 2006

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

IN R Application of Pankaj AGARWAL et al.

Frial No.: 10/562,096

Filing Date: December 21, 2005

For: Biological Data Set Comparison Method

Commissioner for Patents P.O. Box 1450 Alexandria, VA 22313-1450

INFORMATION DISCLOSURE STATEMENT

Applicants request that the references identified on Form PTO-1449 appended hereto be considered by the Examiner and officially made of record in accordance with the provisions of 37 CFR 1.97

	[X]	Copies of the references are enclosed							
	[]	Copies of the references were submitted in parent application Serial No							
		(37 CFR 1.98(d))							
	[] A copy of the International Search Report which issued on International Application No.								
		is submitted herewith. All of the publications cited in the International Search Report							
		are listed on the attached form PTO-1449 and Applicants understand that copies have been							
		supplied to the U.S. Patent Office by the International Bureau.							
A.	[X]	The Information Disclosure Statement submitted herewith is being filed within three							
		months of the filing date of the above application or date of entry into the national stage							
		of an international application or before the mailing date of a first Office action on the							
	٠	merits, whichever event occurs last. 37 CFR 1.97(b).							
	OR								
	[]	The Information Disclosure Statement submitted herewith is being filed before the							
		mailing of a first office action after the filing of a Request For Continued							
		Examination under 37 C.F.R. 1.114 (37 C.F.R. 1.97(b)(4)).							
B.	[]	The Information Disclosure Statement transmitted herewith is being filed after three month							
		of the filing date of the above application or the date of entry into the national stage as set							
		forth in § 1.491 of an international application or after the mailing date of the first Office							
		Action on the merits, whichever event occurred last, but before the mailing date of either:							
		(1) a final action under § 1.113 or							
		(2) a notice of allowance under § 1.311,							
		whichever occurs first.							
		CERTIFICATE OF MAILING (37 CFR 1.8)							
		certify that this paper (along with any referred to as being attached or enclosed) is being deposited with the							
		tates Postal Service on the date shown below with sufficient postage as first class mail in an envelope addressed							
to:	Com	missioner for Patents, PO Box 1450, Alexandria, VA 22313-1450.							
Dat	e:	1/25/2006 Fally Wils							
		Patty Wilson /							

Atty. Docket No. PU4928USw

C.

[]Applicant hereby certifies that each item of information contained in this Information Disclosure Statement was cited in a communication from a foreign patent office in a counterpart foreign application not more than three months prior to the filing of this statement. [] Applicant elects the option to pay the fee set forth in 37 CFR 1.17(p) for submission of an Information Disclosure Statement under § 1.97(c) (\$180.00). The Information Disclosure Statement transmitted herewith is being filed after a final action [] under § 1.113, or a notice of allowance under § 1.311, whichever occurs first, but before the payment of the issue fee. Also enclosed is a copy of the International Search Report which Issued on International Publication No. In accordance with the requirements of 37 CFR 1.97(d): Applicant hereby certifies that each item of information contained in this Information [] Disclosure Statement was cited in a communication from a foreign patent office in a counterpart foreign application not more than three months prior to the filing of this statement. [or] Applicant hereby certifies that no item of information contained in this Information [] Disclosure Statement was cited in a communication from a foreign patent office in a counterpart foreign application, and, to my knowledge after making reasonable inquiry, no item of information contained in this Information Disclosure Statement was known to any individual designated in § 1.56(c) more than three months prior to the filing of this statement; and [] The petition fee set forth in $\S 1.17(i)(1)$ (\$180.00) is submitted herewith.

[] 110 pounou 200 000 202111 111 (1) (1) (1)

[X] Please charge any required fees to Deposit Account No.07-1392.

[] A duplicate copy of this paper is attached.

Respectfully Submitted,

Attorney of Record

Registration No. 37,092

Date: 24 Jan. 2004 Customer No. 23347

GlaxoSmithKline

Corporate Intellectual Property

5 Moore Drive, P.O. Box 13398

Research Triangle Park, NC 27709-3398

Telephone: (919) 483-1012 Facsimile: (919) 483-7988

FILING DATE December 21, 2005 API 2 7 7005 STAPPLICANT Agarwal et al.	FORM PTO	1449				SERIAL NO.		10/562.09	10/562,096			
APPLICANT Agarwal et al.	INFØIOIAT	ION	USCLOSURE ST.	ATEMENT								
EXAMINER U.S. PATENT DOCUMENTS Patent Issue Date Name Class Subclass Faing Date If Appropriate Number Publication Public		E E	6			APPLICANT						
EXAMINER U.S. PATENT DOCUMENTS Patent Issue Date Name Class Subclass Faing Date If Appropriate Number Publication Public	JAN 2	7006	8)									
U.S. PATENT DOCUMENTS Patent Issue Date Name Class Subclass Filing Date Mappropriate	13	1000	أبير									
Patent Number Issue Date Name Class Subclass Mappropriate	103		<u> </u>				OCKET NO.	PU4928U	JSw			
Patent Number Issue Date Name Class Subclass Mappropriate	U.S. PATENT DOCUMENTS											
Document Publication Number Date Country Class Subclass Ves No	Examiner		- '	Issue Date		Name	Class	Subclass				
Document Publication Date Country Class Subclass Ves No												
Document Publication Date Country Class Subclass Ves No												
OTHER DOCUMENTS (Including Author, Title, Journal-Date, Page Number, Etc.) 1. ALTSCHUL et al., Basic Local Alignment Search Tool, J. Mol. Biol. 215:403-410 (1990). 2. AURORA and ROSE, Secking an acient enzyme in Methanococcus jamaschii using ORF, a program based on predicted secondary structure comparisons, Proc. Natl. Acad. Sci. USA 95:281-2823 (1998). 3. BLASCHKE et al., Mining functional information associated with expression arrays, Funct Integr Genomics 1:256-368 (2001). 4. BOUTON and PEVSNER, DRAGON: Database Referencing of Array Genes Online, Bioinformatics 16(11):1038-1039 (2000). 5. BOUTON and PEVSNER, DRAGON View: information visualization for annotated microarray data, Bioinformatics 18(2):323-324 (2002). 6. DEL RIO et al., Mining DNA microarray data using a novel approach based on graph theory, FEBS Letters 509:230-234 (2001). 7. HALUSHKA et al., GIST: A web tool for collecting gene information, Physiol Genomics 1:75-81 (1999). 8. HENIKOFF and HENIKOFF, Amino acid substitution matrices from protein blocks, Proc. Natl. Acad. Sci. USA 89:10915-10919 (1992). 9. JENSSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHARTR et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-336 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identify Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-												
OTHER DOCUMENTS (Including Author, Title, Journal-Date, Page Number, Etc.) 1. ALTSCHUL et al., Basic Local Alignment Search Tool, J. Mol. Biol. 215:403-410 (1990). 2. AURORA and ROSE, Seeking an acient enzyme in Methanococcus jamaschi using ORF, a program based on predicted secondary structure comparisons, Proc. Natl. Acad. Sci. USA 95:2818-2823 (1998). 3. BLASCHKE et al., Mining functional information associated with expression arrays, Funct Integr Genomics 1:256-268 (2001). 4. BOUTON and PEVSNER, DRAGON: Database Referencing of Array Genes Online, Bioinformatics 18(1):1038-1039 (2000). 5. BOUTON and PEVSNER, DRAGON View: information visualization for annotated microarray data, Bioinformatics 18(2):23-23-24 (2002). 6. DBL RIO et al., Mining DNA microarray data using a novel approach based on graph theory, FEBS Letters 509:230-234 (2001). 7. HALUSHKA et al., GIST: A web tool for collecting gene information, Physiol Genomics 1:75-81 (1999). 8. HENIKOFF and HEINKOFF, Amino acid substitution matrices from protein blocks, Proc. Natl. Acad. Sci. USA 89:10915-10919 (1992). 9. JENSSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHATRI et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A combinatorial Partitioning Method to Identity Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11-458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2)-401-						~~~~	Class	Cubalasa				
1. ALTSCHUL et al., Basic Local Alignment Search Tool, J. Mol. Biol. 215:403-410 (1990). 2. AURORA and ROSE, Secking an acient enzyme in Methanococcus jannaschiu sing ORF, a program based on predicted secondary structure comparisons, Proc. Natl. Acad. Sci. USA 95:2818-2823 (1998). 3. BLASCHKE et al., Mining functional information associated with expression arrays, Funct Integr Genomics 1:256-268 (2001). 4. BOUTON and PEVSNER, DRAGON: Database Referencing of Array Genes Online, Bioinformatics 16(11):1038-1039 (2000). 5. BOUTON and PEVSNER, DRAGON View: information visualization for annotated microarray data, Bioinformatics 18(2):323-324 (2002). 6. DEL RIO et al., Mining DNA microarray data using a novel approach based on graph theory, FEBS Letters 509:230-234 (2001). 7. HALUSHKA et al., GIST: A web tool for collecting gene information, Physiol Genomics 1:75-81 (1999). 8. HENIKOFF and HENIKOFF, Amino acid substitution matrices from protein blocks, Proc. Natl. Acad. Sci. USA 89:10915-10919 (1992). 9. JENSSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHARIR et al., Proling Gene Expression Using Ontoe-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identity Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON and LIPMAN, improved tools for biological sequence			Number	Date	•	Jountry	Class	Subciass				
1. ALTSCHUL et al., Basic Local Alignment Search Tool, J. Mol. Biol. 215-633-410 (1990). 2. AURORA and ROSE, Secking an acient enzyme in Methanococcus jamnaschii using ORF, a program based on predicted secondary structure comparisons, Proc. Natl. Acad. Sci. USA 95:2818-2823 (1998). 3. BLASCHKE et al., Mining functional information associated with expression arrays, Funct Integr Genomics 1:256-268 (2001). 4. BOUTON and PEVSNER, DRAGON: Database Referencing of Array Genes Online, Bioinformatics 16(11):1038-1039 (2000). 5. BOUTON and PEVSNER, DRAGON View: information visualization for annotated microarray data, Bioinformatics 18(2):323-324 (2002). 6. DEL RIO et al., Mining DNA microarray data using a novel approach based on graph theory, FEBS Letters 509-230-234 (2001). 7. HALUSHKA et al., GIST: A web tool for collecting gene information, Physiol Genomics 1:75-81 (1999). 8. HENIKOFF and HENIKOFF, Amino acid substitution matrices from protein blocks, Proc. Natl. Acad. Sci. USA 89:10915-10919 (1992). 9. JENSSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 282-12-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHARIR et al., Proling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchics to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identity Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON and LiPMAN, Improved tools for biological sequence				7								
1. ALTSCHUL et al., Basic Local Alignment Search Tool, J. Mol. Biol. 215:403-410 (1990). 2. AURORA and ROSE, Secking an acient enzyme in Methanococcus jannaschiu sing ORF, a program based on predicted secondary structure comparisons, Proc. Natl. Acad. Sci. USA 95:2818-2823 (1998). 3. BLASCHKE et al., Mining functional information associated with expression arrays, Funct Integr Genomics 1:256-268 (2001). 4. BOUTON and PEVSNER, DRAGON: Database Referencing of Array Genes Online, Bioinformatics 16(11):1038-1039 (2000). 5. BOUTON and PEVSNER, DRAGON View: information visualization for annotated microarray data, Bioinformatics 18(2):323-324 (2002). 6. DEL RIO et al., Mining DNA microarray data using a novel approach based on graph theory, FEBS Letters 509:230-234 (2001). 7. HALUSHKA et al., GIST: A web tool for collecting gene information, Physiol Genomics 1:75-81 (1999). 8. HENIKOFF and HENIKOFF, Amino acid substitution matrices from protein blocks, Proc. Natl. Acad. Sci. USA 89:10915-10919 (1992). 9. JENSSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHARIR et al., Proling Gene Expression Using Ontoe-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identity Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON and LIPMAN, improved tools for biological sequence	OTHER DOCUMENTS (Including Author Title Journal Date Page Number Etc.)											
2. AURORA and ROSE, Seeking an acient enzyme in Methanococcus jannaschii using ORF, a program based on predicted secondary structure comparisons, Proc. Natl. Acad. Sci. USA 95:2818-2823 (1998). 3. BLASCHKE et al., Mining functional information associated with expression arrays, Funct Integr Genomics 1:256-268 (2001). 4. BOUTON and PEVSNER, DRAGON: Database Referencing of Array Genes Online, Bioinformatics 16(11):1038-1039 (2000). 5. BOUTON and PEVSNER, DRAGON View: information visualization for annotated microarray data, Bioinformatics 18(2):323-324 (2002). 6. DEL RIO et al., Mining DNA microarray data using a novel approach based on graph theory, FEBS Letters 509:230-234 (2001). 7. HALUSHKA et al., GIST: A web tool for collecting gene information, Physiol Genomics 1:75-81 (1999). 8. HENIKOFF and HENIKOFF, Amino acid substitution matrices from protein blocks, Proc. Natl. Acad. Sci. USA 99:10915-10919 (1992). 9. JENSSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHATRI et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved to												
on predicted secondary structure comparisons, Proc. Natl. Acad. Sci. USA 95:2818-2823 (1998). 3. BLASCHKE et al., Mining functional information associated with expression arrays, Funct Integr Genomics 1:256-268 (2001). 4. BOUTON and PEVSNER, DRAGON: Database Referencing of Array Genes Online, Bioinformatics 16(1):1038-1039 (2000). 5. BOUTON and PEVSNER, DRAGON View: information visualization for annotated microarray data, Bioinformatics 18(2):323-324 (2002). 6. DEL RIO et al., Mining DNA microarray data using a novel approach based on graph theory, FEBS Letters 509:230-234 (2001). 7. HALUSHKA et al., GIST: A web tool for collecting gene information, Physiol Genomics 1:75-81 (1999). 8. HENIKOFF and HENIKOFF, Amino acid substitution matrices from protein blocks, Proc. Natl. Acad. Sci. USA 89:10915-10919 (1992). 9. JENSSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHATRI et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 18:36-398 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IR												
3. BLASCHKE et al., Mining functional information associated with expression arrays, Funct Integr Genomics 1:256-268 (2001). 4. BOUTON and PEVSNER, DRAGON: Database Referencing of Array Genes Online, Bioinformatics 16(11):1038-1039 (2000). 5. BOUTON and PEVSNER, DRAGON View: information visualization for annotated microarray data, Bioinformatics 18(2):323-324 (2002). 6. DEL RIO et al., Mining DNA microarray data using a novel approach based on graph theory, FEBS Letters 509:230-234 (2001). 7. HALUSHKA et al., GIST: A web tool for collecting gene information, Physiol Genomics 1:75-81 (1999). 8. HENIKOFF and HENIKOFF, Amino acid substitution matrices from protein blocks, Proc. Natl. Acad. Sci. USA 89:10915-10919 (1992). 9. JENSSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHATRI et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-38 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotech												
1:256-268 (2001). 4. BOUTON and PEVSNER, DRAGON: Database Referencing of Array Genes Online, Bioinformatics 16(11):1038-1039 (2000). 5. BOUTON and PEVSNER, DRAGON View: information visualization for annotated microarray data, Bioinformatics 18(2):323-324 (2002). 6. DEL RIO et al., Mining DNA microarray data using a novel approach based on graph theory, FEBS Letters 592:30-234 (2001). 7. HALUSHKA et al., GIST: A web tool for collecting gene information, Physiol Genomics 1:75-81 (1999). 8. HENIKOFF and HENIKOFF, Amino acid substitution matrices from protein blocks, Proc. Natl. Acad. Sci. USA 89:10915-10919 (1992). 9. JENSSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHATRI et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 18:36-398 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATYETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATYETA et al., Computing Fuzzy Associations for the Analysis of B												
16(11):1038-1039 (2000). 5. BOUTON and PEVSNER, DRAGON View: information visualization for annotated microarray data, Bioinformatics 18(2):323-324 (2002). 6. DEL RIO et al., Mining DNA microarray data using a novel approach based on graph theory, FEBS Letters 509:230-234 (2001). 7. HALUSHKA et al., GIST: A web tool for collecting gene information, Physiol Genomics 1:75-81 (1999). 8. HENIKOFF and HENIKOFF, Amino acid substitution matrices from protein blocks, Proc. Natl. Acad. Sci. USA 89:10915-10919 (1992). 9. JENSSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHATRI et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identity Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-			1:256-268 (2001).									
5. BOUTON and PEVSNER, DRAGON View: information visualization for annotated microarray data, Bioinformatics 18(2):323-324 (2002). 6. DEL RIO et al., Mining DNA microarray data using a novel approach based on graph theory, FEBS Letters 509:230-234 (2001). 7. HALUSHKA et al., GIST: A web tool for collecting gene information, Physiol Genomics 1:75-81 (1999). 8. HENIKOFF and HENIKOFF, Amino acid substitution matrices from protein blocks, Proc. Natl. Acad. Sci. USA 89:10915-10919 (1992). 9. JENSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHATRI et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trair Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:244-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order In		4.			ON: Databa	ase Referencing of	Array Genes (Online, Bioinf	ormatics			
Bioinformatics 18(2):323-324 (2002). 6. DEL RIO et al., Mining DNA microarray data using a novel approach based on graph theory, FEBS Letters 509:230-234 (2001). 7. HALUSHKA et al., GIST: A web tool for collecting gene information, Physiol Genomics 1:75-81 (1999). 8. HENIKOFF and HENIKOFF, Amino acid substitution matrices from protein blocks, Proc. Natl. Acad. Sci. USA 89:10915-10919 (1992). 9. JENSSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHATRI et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. McGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 19. PEREZ-IRATXETA et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Gen	16(11) :1038-1039 (2000).							-				
6. DEL RIO et al., Mining DNA microarray data using a novel approach based on graph theory, FEBS Letters 509:230-234 (2001). 7. HALUSHKA et al., GIST: A web tool for collecting gene information, Physiol Genomics 1:75-81 (1999). 8. HENIKOFF and HENIKOFF, Amino acid substitution matrices from protein blocks, Proc. Natl. Acad. Sci. USA 89:10915-10919 (1992). 9. JENSSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHATRI et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). E									rray data,			
509:230-234 (2001). 7. HALUSHKA et al., GIST: A web tool for collecting gene information, Physiol Genomics 1:75-81 (1999). 8. HENIKOFF and HENIKOFF, Amino acid substitution matrices from protein blocks, Proc. Natl. Acad. Sci. USA 89:10915-10919 (1992). 9. JENSSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHATRI et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identity Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with M							1. 1 1	1. 41	EEDG I			
7. HALUSHKA et al., GIST: A web tool for collecting gene information, Physiol Genomics 1:75-81 (1999). 8. HENIKOFF and HENIKOFF, Amino acid substitution matrices from protein blocks, Proc. Natl. Acad. Sci. USA 89:10915-10919 (1992). 9. JENSSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHATRI et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 18:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line thr												
8. HENIKOFF and HENIKOFF, Amino acid substitution matrices from protein blocks, Proc. Natl. Acad. Sci. USA 89:10915-10919 (1992). 9. JENSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHATRI et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance		7			tool for call	lecting gene inform	ation Physiol	Genomics 1:	75 81 (1000)			
USA 89:10915-10919 (1992). 9. JENSSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHATRI et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through												
9. JENSSEN et al., A literature network of human genes for high-throughput analysis of gene expression, Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHATRI et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2442-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through												
Nature Genetics 28:21-28 (2001). 10. KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHATRI et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identity Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through		9.			rk of huma	n genes for high-th	roughput anal	ysis of gene e	xpression,			
sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993). 11. KHATRI et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through												
11. KHATRI et al., Profiling Gene Expression Using Onto-Express, Genomics 79(2):266-270 (2002). 12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through		10.	KARLIN and ALTSCHUL, Applications and statistics for multiple high-scoring segments in molecular									
12. MASYS et al., Use of keyword hierarchies to interpret gene expression patterns, Bioinformatics 17(4):319-326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through			sequences, Proc. Natl. Acad. Sci. USA 90:5873-5877 (1993).									
326 (2001). 13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through												
13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Function and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through												
and Genetics 48:44-52 (2002). 14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through	13. MCGUFFIN and JONES, Targeting Novel Folds for Structural Genomics, PROTEINS: Structure, Fun and Genetics 48:44-52 (2002).								-t			
14. NELSON et al., A Combinatorial Partitioning Method to Identigy Multilocus Genotypic Partitions that Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expresion Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through									cture, Function			
Predict Quantitative Trait Variation, Genome Research 11:458-470 (2001). 15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through									ritions that			
15. PAVLIDIS et al., Learning Gene Functional Classifications from Multiple Data Types, J. of Computational Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through												
Biology 9(2):401-411 (2002). 16. PEARSON, Rapid and Sensitive Sequence Comparison with FASTP and FASTA, Methods in Enzymology 183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expresion Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through												
183:63-98 (1990). 17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through							<u> </u>		<u>.</u>			
17. PEARSON and LIPMAN, Improved tools for biological sequence comparison, Proc. Natl. Acad. Sci. USA 85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through									n Enzymology			
85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through	183 :63-98 (1990).											
18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining, Nature Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expresion Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through	85:2444-2448 (1988). 18. PEREZ-IRATXETA et al., Association of genes to genetically inherited diseases using data mining,								cad. Sci. USA			
Genetics 31:316-319 (2002). 19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen- Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through												
19. PEREZ-IRATXETA et al., Computing Fuzzy Associations for the Analysis of Biological Literature, Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen- Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through									mınıng, Nature			
Biotechniques 32:1380-1385 (2002). 20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through												
20. RITCHIE et al., Multifactor-Dimensionality Reduction Reveals High-order Interations among Estrogen-Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through												
Metabolism Genes in Sporadic Breast Cancer, Am. J. Hum. Genet. 69:138-147 (2001). 21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through												
21. TANABE et al., Medminer: An internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through	l											
Gene Expresion Profiling, Biotechniques 27:1210-1217 (1999). EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through									Application to			
EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP § 609; Draw line through												
	EXAMINER						DATE	CONSIDERE	D			
	EVAMINED.	Initia	l if citation consider	red whether or -	not citation	is in conformance -	with MDED 9	600: Dea 1:	a through			